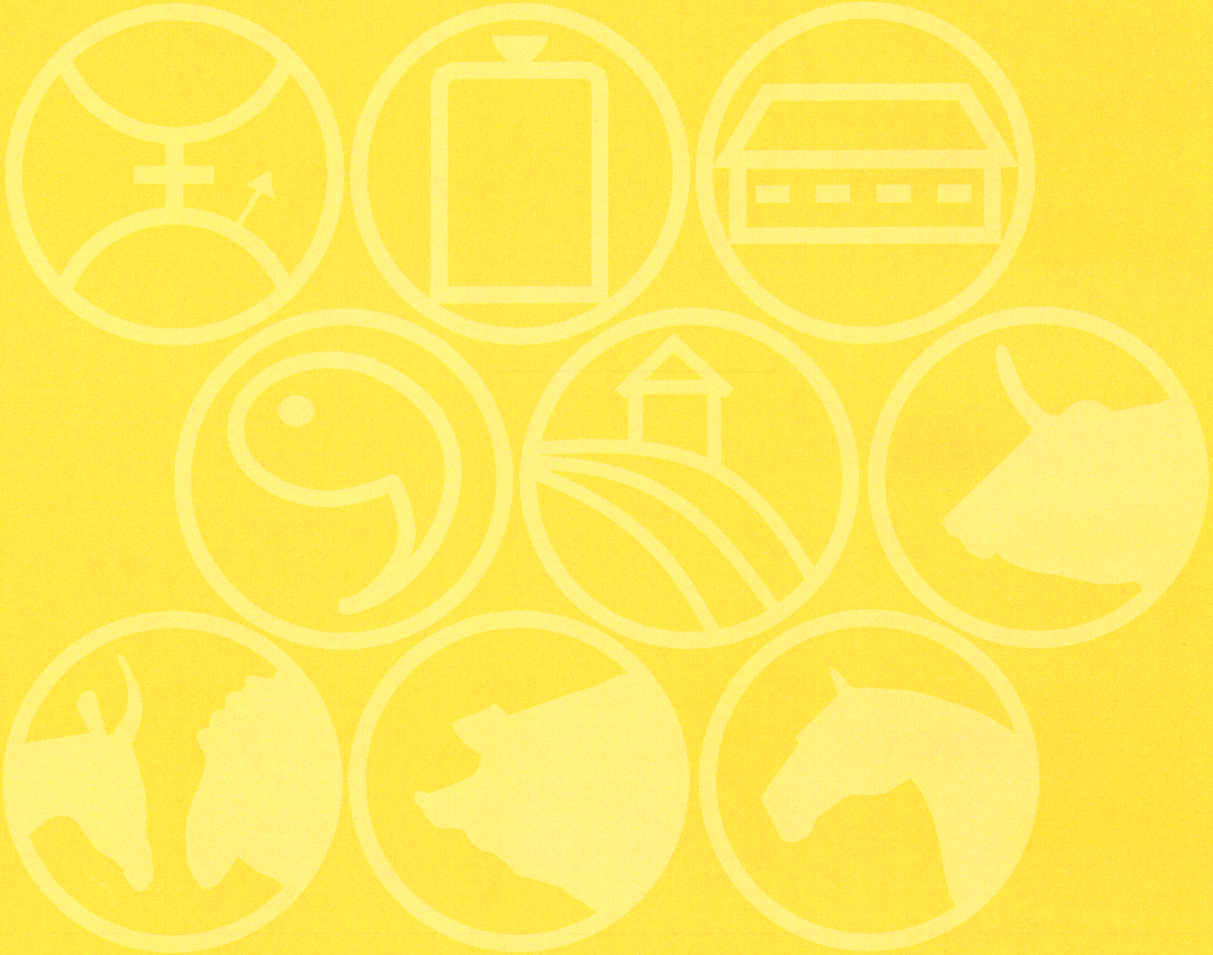
Genomic Selection to reduce Boar Taint in Danish Pigs

Strathe, Anders Bjerring; Mark, Thomas; Velander, I. H.; Kadarmideen, Haja

Book of Abstracts of the 65th Annual Meeting of the European Federation of Animal Science



Book of abstracts No. 20 (2014)
Copenhagen, Denmark
25 - 29 August 2014

Book of Abstracts of the 65th Annual Meeting of the European Federation of Animal Science

Genomic selection to reduce boar taint in Danish pigs

A.B. Strathe[1,2], T. Mark[2], I.H. Velander[1] and H.N. Kadarmideen[2]
[1]Pig Research Centre, Department of Breeding and Genetics, Axeltorv 3, 1609 Copenhagen V, Denmark, [2]University of Copenhagen, Department of Clinical Veterinary and Animal Sciences, Groennegaardsvej 3, 1870 Frederiksberg C, Denmark; strathe@sund.ku.dk

Producer and animal welfare organizations within EU have signed a voluntary declaration to stop castration by 2018. Hence, developing a genetic solution to boar taint (BT) is of key interest. The aim of this work was to develop genomic selection and phenotyping scheme against BT for all 3 Danish pig breeds, and to present preliminary results from the ongoing geno- and phenotyping. A performance test for BT has been developed, where the main chemical compounds and a human-nose score (HNS) of boar taint were recorded on either live male breeding candidates or slaughter boars. Using the Danish Duroc as an example, concentrations of androstenone (AND) and skatole (SKA) in the back fat was currently available for approximately 700 boars while 2,192 boars were recorded for HNS. Furthermore, 396 boars with BT phenotypes had genotype information (60K SNP chip). Heritabilities of HNS, log(AND) and log(SKA), estimated using a multi-trait single-step GBLUP model, were 0.12, 0.55 and 0.17, respectively. The most notable genetic correlation was between HNS and log(AND), being 0.55. Genetic correlations between log(AND) and litter size and semen traits suggest currently that selection against BT will have minimal impact on fertility. The association analysis with 33028 SNPs revealed that log(AND) levels in fat tissue were significantly affected by 31 SNPs on pig chromosomes SSC1 and SSC6. On SSC6, a larger region of 10 Mb was shown to be associated with log(AND) covering several candidate genes potentially involved in the synthesis and metabolism of androgens. In summary, the project uses genomics for aiding a future meat production of meat from entire males, being free of boar taint so that consumers will continue to appreciate an odorless meatball.

Model comparison based on genomic predictions of litter size and piglet mortality

X. Guo[1], O.F. Christensen[1], T. Ostersen[2], D.A. Sorensen[1], Y. Wang[3], M.S. Lund[1] and G. Su[1]
[1]Aarhus University, Dept. of Molecular Biology and Genetics, Blichers Allé 20, 8830 Tjele, Denmark, [2]Pig Research Centre, Danish Agricultural and Food Council, Axeltorv 3, 1609 Copenhagen, Denmark, [3]China Agricultural University, Dept. of Animal Science and Technology, Yuanmingyuan West Road No. 2, 100193 Beijing, China, P.R.; xiangyu.guo@agrsci.dk

Prediction of breeding values (BV) based on dense markers across the genome has become an important component of pig breeding programs. This study compared traditional BLUP, genomic BLUP (GBLUP), and single-step models for genomic predictions of litter size and piglet mortality in the Danish Landrace and Yorkshire populations. The data consisted of 778,095 records of 309,362 Landrace and 472,001 records of 190,760 Yorkshire sows. There were 332,795 Landrace and 207,255 Yorkshire animals in the pedigree, among which 3,445 (1,366 boars and 2,079 sows) Landrace and 3,372 (1,241 boars and 2,131 sows) Yorkshire individuals were genotyped. To validate prediction reliability, the data were divided into a training dataset (80%, born before 2012-04-01) and a validating dataset (20%). The traits were total number of piglets born (TNB), litter size at five days after birth (LS5) and mortality rate before day 5 (Mort). BV were predicted using a traditional BLUP model with pedigree-based relationship matrix, a GBLUP model with marker-based relationship matrix, and a single-step model with a combined relationship matrix constructed from marker and pedigree information. The reliabilities of estimated breeding values (EBV) were computed as the squared correlation between EBV and corrected phenotypic value (y_c), divided by the heritability of y_c. In general, the single-step model predicted EBV more accurately than the GBLUP model, and the latter in turn better than the traditional BLUP. The results indicate that genomic information can increase the reliabilities of predictions of litter size and piglet mortality, and that the single-step model is a useful tool for practical genomic prediction.